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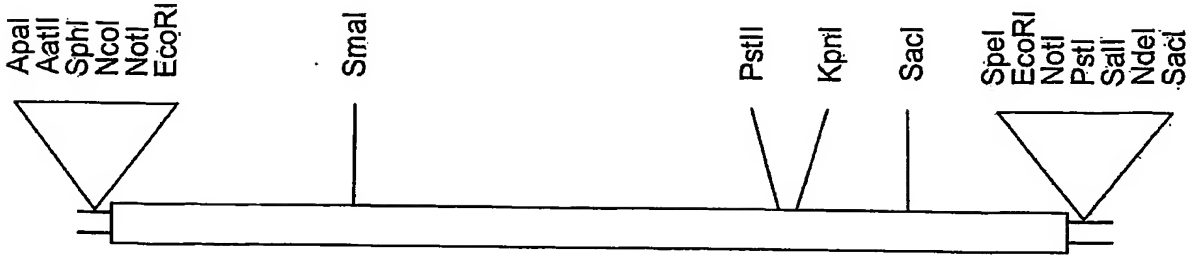

TrCHSa3

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FIGURE 1

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   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
  51 AAAAACAACT ACGCATATTA TATATATATA TATATAGTCT ATAATTGAAA
 101 GAAACTGCTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTCGC
 151 AAGGCTCAGA GGGCTGAAGG CCCTGCAACC ATTTTGGCCA TTGGCACTGC
 201 AAATCCACCA AACCGTGTTG AGCAGAGCAC ATATCCTGAT TTCTACTTCA
 251 AAATTACAAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
 301 ATGTGTGACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
 351 GATTTTGAAA GAAAATCCTA GTCTTTGTGA ATACATGGCA CCTTCATTGG
 401 ATGCTAGGCA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
 451 GCTGCAGTCA AGGCCATTAA AGAATGGGGT CAACCAAAGT CAAAGATTAC
 501 TCACTTAATC TTTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
 551 ACCAACTCAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
 601 ATGTACCAAC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTTGGCAAA
 651 AGATTTGGCC GAGAACAACA AAGGTGCTCG TGTGCTAGTT GTTTGTTCTG
 701 AAGTCACCGC AGTCACATTT CGCGGCCCCA GTGATACTCA CTTGGACAGT
 751 CTTGTTGGAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
 801 TTCTGATCCA GTGCCTGAAA TTGAGAAACC AATATTTGAG ATGGTTTGGA
 851 CTGCACAAAC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
 901 CGTGAAGCTG GGCTAACATT TCATCTTCTT AAAGATGTTC CTGGGATTGT
 951 ATCAAAGAAC ATTAATAAAG CATTGGTTGA GGCTTTCCAA CCATTAGGAA
1001 TTTCTGACTA CAACTCAATC TTTTGGATTG CACACCCGGG TGGACCTGCA
1051 ATTCTTGATC AAGTAGAACA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 GGCCACGAGG GAAGTTCTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 TATTGTTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 AAGACAACTG GAGAAGGACT TGATTGGGGT GTGTTGTTCG GCTTCGGACC
1251 AGGACTTACC ATTGAAACCG TTGTTCTTCG TAGCGTGGCT ATATAAGATG
1301 TGTGATTGTT TTTATTTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 TTCGATTTAA GAATAAATAA ATATATCTTT TGATAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTC
```

FIGURE 2

```
  1 MVSVAEIRKA QRAEGPATIL AIGTANPPNR VEQSTYPDFY FKITNSEHKT
 51 ELKEKFQRMC DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSLV GQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYNSIFW
301 IAHPGGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKSAQNGLKT TGEGLDWGVL FGFGPGLTIE TVVLRSVAI
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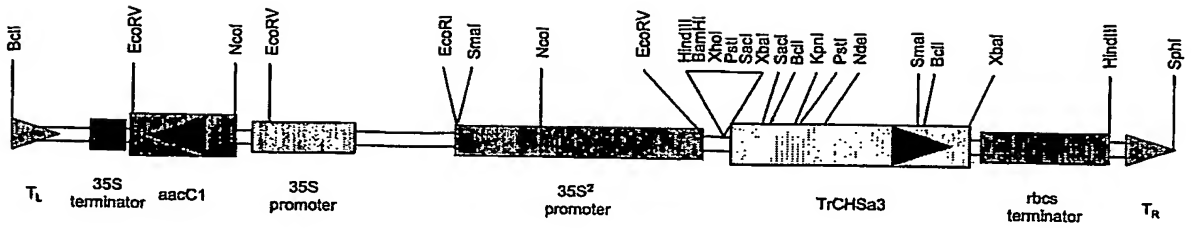
FIGURE 3



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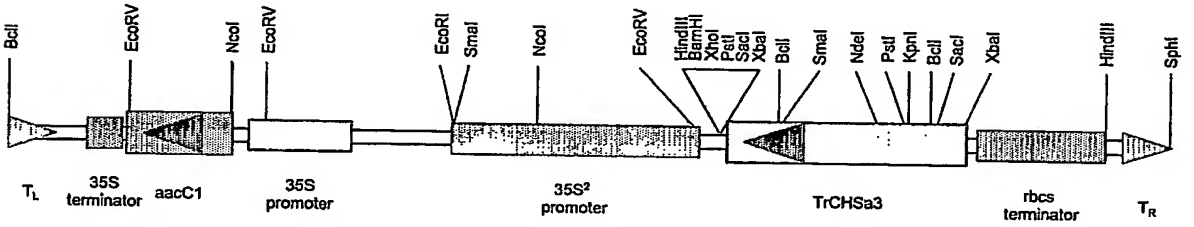

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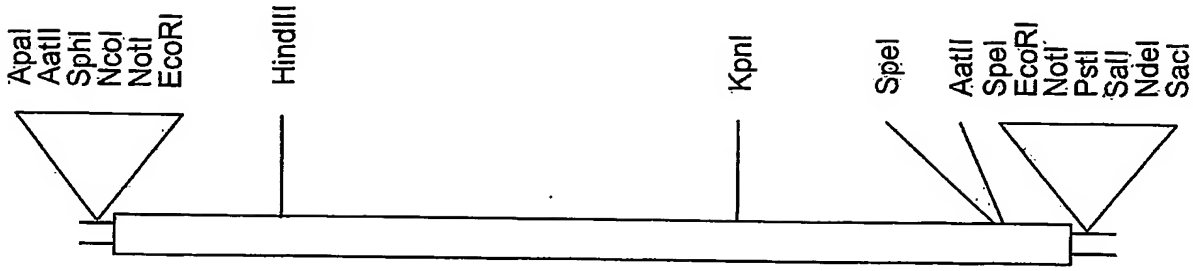
FIGURE 4



TrCHSc

FIGURE 5

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   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATTCAATCT
  51 GTTGTGCATA AAATTCACTC ATTGCATAGA AAACCATACA CATTTGATCT
 101 TGCAAAGAAG AAATATGGGA GACGAAGGTA TAGTGAGAGG TGTCACAAAG
 151 CAGACAACCC CTGGGAAGGC TACTATATTG GCTCTTGGCA AGGCATTCCC
 201 TCACCAACTT GTGATGCAAG AGTGTTTAGT TGATGGTTAT TTTAGGGACA
 251 CTAATTGTGA CAATCCTGAA CTTAAGCAGA AACTTGCTAG ACTTTGTAAG
 301 ACAACCACGG TAAAAACAAG GTATGTTGTT ATGAATGAGG AGATACTAAA
 351 GAAATATCCA GAACTTGTTG TCGAAGGCGC CTCAACTGTA AAACAACGTT
 401 TAGAGATATG TAATGAGGCA GTAACACAAA TGGCAATTGA AGCTTCCCAA
 451 GTTTGCCTAA AGAATTGGGG TAGATCCTTA TCGGACATAA CTCATGTGGT
 501 TTATGTTTCA TCTAGTGAAG CTAGATTACC CGGTGGTGAC CTATACTTGT
 551 CAAAAGGACT AGGACTAAAC CCTAAAATTC AAAGAACCAT GCTCTATTTC
 601 TCTGGATGCT CGGGAGGCGT AGCCGGCCTT CGCGTTGCGA AAGACGTAGC
 651 TGAGAACAAC CCTGGAAGTA GAGTTTTGCT TGCTACTTCG GAAACTACAA
 701 TTATTGGATT CAAGCCACCA AGTGTTGATA GACCTTATGA TCTTGTTGGT
 751 GTGGCACTCT TTGGAGATGG TGCTGGTGCA ATGATAATTG GCTCAGACCC
 801 GGTATTTGAA ACTGAGACAC CATTGTTTGA GCTGCATACT TCAGCTCAGG
 851 AGTTTATACC AGACACCGAG AAGAAAATTG ATGGGCGGCT GACGGAGGAG
 901 GGCATAAGTT TCACACTAGC AAGGGAACTT CCGCAGATAA TCGAAGACAA
 951 TGTTGAGGGA TTCTGTAATA AACTAATTGA TGTTGTTGGG TTGGAGAATA
1001 AGGAGTACAA TAAGTTGTTT TGGGCTGTGC ATCCAGGTGG GCCTGCGATA
1051 TTGAATCGCG TGGAGAAGCG GCTTGAGTTG TCGCCGCAGA AGCTGAATGC
1101 TAGTAGAAAA GCTCTAATGG ATTATGGAAA TGCTAGCAGC AATACTATTG
1151 TTTATGTGCT GGAATATATG CTAGAAGAGG AAAAGAAGAT TAAAAAGGCG
1201 GGTGGAGGAG ATTCTGAATG GGGATTGATA CTTGCTTTTG GACCTGGAAT
1251 TACTTTTGAG GGGATTCTAG CAAGGAACTT GTGTGCATGA AGTCTTATAC
1301 AATTGTGATG CATGACTTAT ACTCTTATTT CTACTAATTA TTATATTAAG
1351 CAAATTCAGA ACTTTTAAGT AATGATTTAA TGAAGAATAC TTATAGTATA
1401 TTGACTTTAT TCACTTTCAA AGCAAGTTTA TGATCCTAAG ACATGGTAGA
1451 ACTTGAGCAT GTGGAATAGT TGTAACAAAA ACTCTAAGCA AATAGAGACT
1501 TTATGTAGTA TAAAGCATTT CCAGACATGA TAAATAATGG TACCTCAGAA
1551 CATAAAATAT ATTTAGCTAT CTTTCATCCC CAACTTTACA CATCCACCAA
1601 GGTACAGAAT AAGCATATGT CAACACAAAA TGTACTCTAA GTCTAACATG
1651 AGTAACCAAA CATGATGCCT GATTAAGTTA AAAGAAAAGA AAATCTGAGG
1701 GCATAGATCT TCAATCACAC CACTCCAGAG GGAAGGCGTA GAACAAGCTG
```

FIGURE 6

1751 TCCGCCGAAA ACACTGCAAT TCAATAAATA TCATTAGGAC AACAGTGCAG
1801 AGTCATGCGG GAAATGTCTT AAGTCACTGT ACTAAAAATA TAGGATTATA
1851 TTATGAACTA TACTAACCTT TTCACATAAT AGTAACAGAA ATCAGCTAAG
1901 ATGAATGTCT GGACAATTTC TGAGATAAGA ACCATGACGG CCATAAGCCA
1951 TACCCCAAGG CAACCAATAA ATGTCCACGG GTATCTAACA CCTGTTGCAA
2001 GAAATAGTAA GTTATTAGGA GATGTGCGGT TACGAAATTC AAGCTACACA
2051 ACAAAAGGAG GCCAGAACAA CAGCAATCTT GTAACCAGAT GACAACAATA
2101 AAATGTAAAC TTAAAGAGAC CGAACACACA AACATTGCAA CTCAGATGGA
2151 ATTGCTGCCA TGTAACTAGT AGGAGATTTG GGACGTCAAA TCAGTATATT
2201 ATGCAAATAC AAGGTATGAC CGCCTTGTCT ATTGTAGCAT ACAACAAACG
2251 TACAGTGGGT TTGTCCCTCT CAAAATGGCA GGATCTTTAC AGCACAATAT
2301 TTGGTTTTGT CATACTTATA CCATAAAAAA AAAAAAAAAA AAAAAAAAAA
2351 AAAGTACTCT GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC

FIGURE 6 (cont.)

```
  1 MGDEGIVRGV TKQTTPGKAT ILALGKAFPH QLVMQECLVD GYFRDTNCDN
 51 PELKQKLARL CKTTTVKTRY VVMNEEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQRTML YFSGCSGGVA GLRVAKDVAE NNPGSRVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNA SSNTIVYVLE
351 YMLEEEKKIK KAGGGDSEWG LILAFGPGIT FEGILARNLC A
```

FIGURE 7

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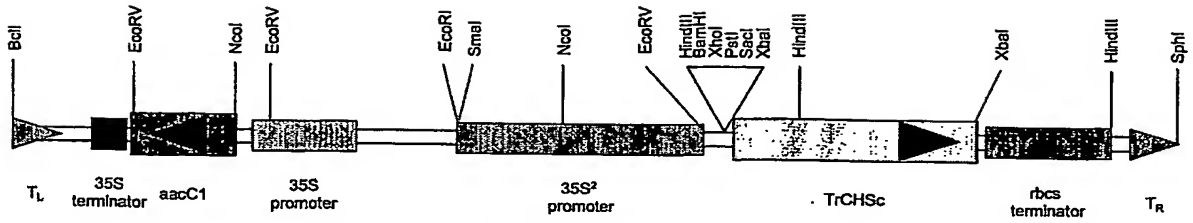

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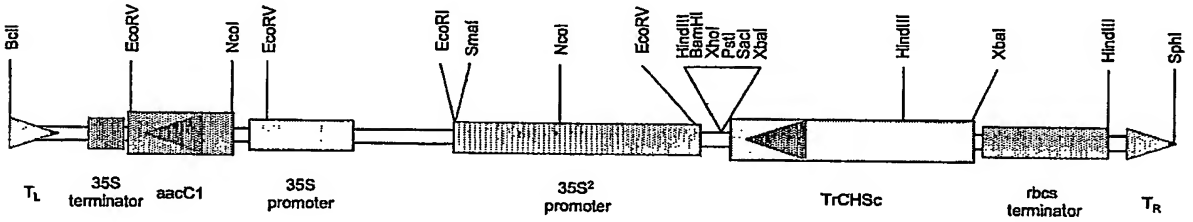

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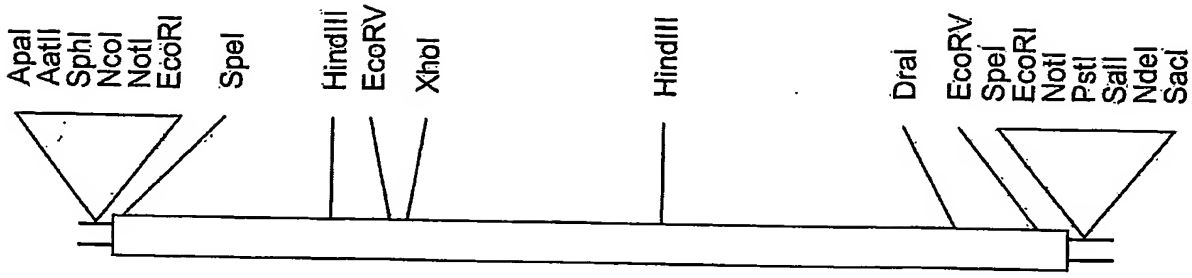
FIGURE 8



TrCHSf

FIGURE 9

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG ACTAAGCCTT
  51 GATTCATTGT TTGTTTCCAT AACACAAGAA CTAGTGTTTG CTTGAATCTT
 101 AAGAAAAAAT GCCTCAAGGT GATTTGAATG GAAGTTCCTC GGTGAATGGA
 151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCATT
 201 AGGAAAGGCT TTCCCCGCCC AGGTCCTCCC TCAAGAGTGC TTGGTGGAAG
 251 GATTCATTCG CGACACTAAG TGTGACGATA CTTATATTAA GGAGAAATTG
 301 GAGCGTCTTT GCAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
 351 AAAGGAGATC TTAGACAACT ATCCAGAGCT AGCCATAGAT GGAACACCAA
 401 CAATAAGGCA AAAGCTTGAA ATAGCAAATC CAGCAGTAGT TGAAATGGCA
 451 ACAAGAGCAA GCAAAGATTG CATCAAAGAA TGGGGAAGGT CACCTCAAGA
 501 TATCACACAC ATAGTCTATG TTTCCTCGAG CGAAATTCGT CTACCCGGTG
 551 GTGACCTTTA TCTTGCAAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
 601 GTAATGCTCT ATTTCCTCGG TTGCTACGGC GGTGTCACTG GCTTACGTGT
 651 CGCCAAAGAC ATCGCCGAAA ATAACCCTGG TAGTAGGGTG TTACTCACAA
 701 CATCCGAGAC CACTATTCTC GGTTTTCGAC CACCGAGTAA AGCTAGACCT
 751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
 801 AATTGGAACA GACCCTATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
 851 ACCATGCAGT CCAAAAATTC TTGCCTGATA CACAAAATGT GATTGATGGT
 901 AGAATCACTG AAGAGGGTAT TAATTTTAAG CTTGGAAGAG ACCTTCCTCA
 951 AAAAATTGAA GACAATATTG AAGAATTTTG CAAGAAAATT ATGGCTAAAA
1001 GTGATGTTAA GGAATTTAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
1101 ATTGGATTGT AGTAGGAAGG CATTAATGGA TTATGGAAAT GTTAGTAGCA
1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
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1451 TTTAAGTTCT TGACCATACT GATTTTTTCT TTACACATTT TCATATCTAA
1501 AATTGTTCTA TGATATCTTC ATTGTTGATA CTGTAATAAT ATAATATCTA
1551 ATTTGGCTGG CAAAATGAAA GATTTTTCAC CGAAAAAAAA AAAAAAAAAA
1601 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
1651 TTC
```

FIGURE 10

```
  1  MPQGDLNGSS SVNGARARRA PTQGKATILA LGKAFPAQVL PQECLVEGFI
 51  RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGTPTIR
101  QKLEIANPAV VEMATRASKD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151  YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201  TTILGFRPPS KARPYDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251  VQKFLPDTQN VIDGRITEEG INFKLGRDLP QKIEDNIEEF CKKIMAKSDV
301  KEFNDLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351  FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL
```

FIGURE 11

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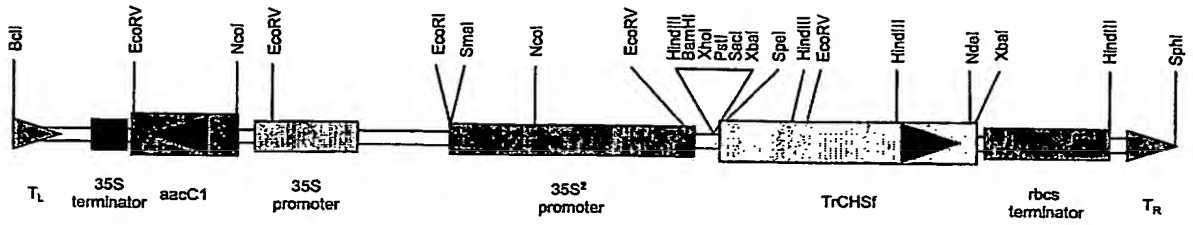

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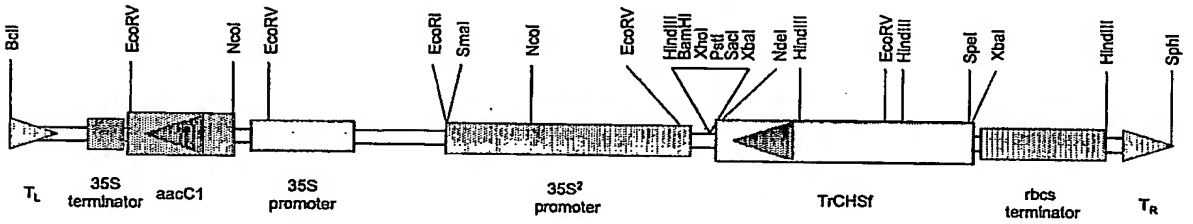

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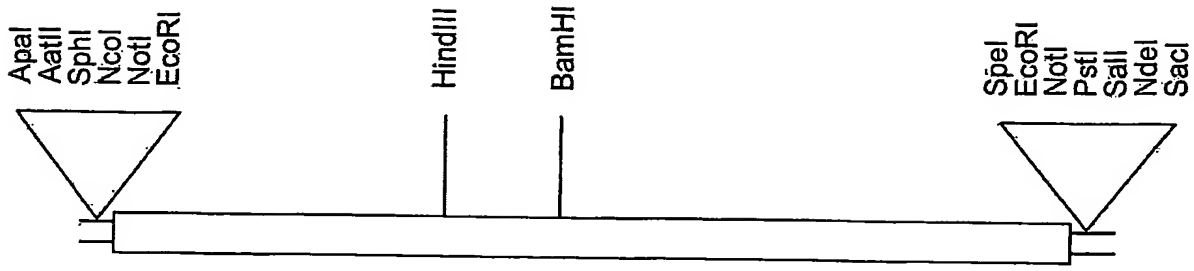
FIGURE 12



TrCHSh

FIGURE 13

```
   1 GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGAA
  51 TCCACCAAAT CAACACCATT AATAACCTTC CAAATTCTCG TTACCTCACC
 101 AAATCTCATT TTTCATTATA TATCTTGGGT ACATCTTTTG TTACCTCCAA
 151 CAAAAAAATG GTGACCGTAG AAGAGATTCG TAACGCCCAA CGTTCAAATG
 201 GCCCTGCCAC TATCTTAGCT TTTGGCACAG CCACTCCTTC TAACTGTGTC
 251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACCA ACAGCGAACA
 301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
 351 TAAAGAAACG TTACATGCAC CTAACAGAAG ACTTTCTGAA GGAGAATCCA
 401 AATATGTGTG AATACATGGC ACCATCACTA GATGTAAGAC GAGACATAGT
 451 GGTTGTTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
 501 GTGAATGGGG ACAACCAAAA TCCAAAATCA CACATCTTGT TTTCTGCACC
 551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAAACTTTT
 601 AGGCTTAAAA CCTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
 651 TCGCTGGCGG CACAGTTCTC CGCTTAGCAA AAGACCTTGT TGAGAATAAC
 701 AAAAATGCAA GAGTTCTTGT TGTTTGTTCT GAAATTACTG CGGTTACTTT
 751 TCGTGGACCA TCGGATACTC ATCTTGATTC GCTCGTGGGA CAGGCGCTTT
 801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAACC
 851 GTGGAGCGTC CGATTTTCGA GATTGTTTCG GCTGCTCAGA CTATTCTTCC
 901 TGATTCTGAT GGCGCAATTG ATGGACATCT TCGTGAAGTG GGGCTCACTT
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1001 AGTTTAGTTG AAGCTTTTGC GCCTATTGGG ATTAATGATT GGAACTCAAT
1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTTAGAC CAGGTTGAAG
1101 AGAAACTCCA TCTTAAAGAG GAGAAACTCC GGTCCACCCG GCATGTGCTT
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```

FIGURE 14

```
  1  MVTVEEIRNA QRSNGPATIL AFGTATPSNC VTQADYPDYY FRITNSEHMT
 51  DLKEKFKRMC DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIVVV
101  EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMPGA DYQLTKLLGL
151  KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201  PSDTHLDSLV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTILPDS
251  DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301  VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351  KRSKEEGMIT TGEGLEWGVL FGFGPGLTVE TVVLHSVPVQ G
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FIGURE 15

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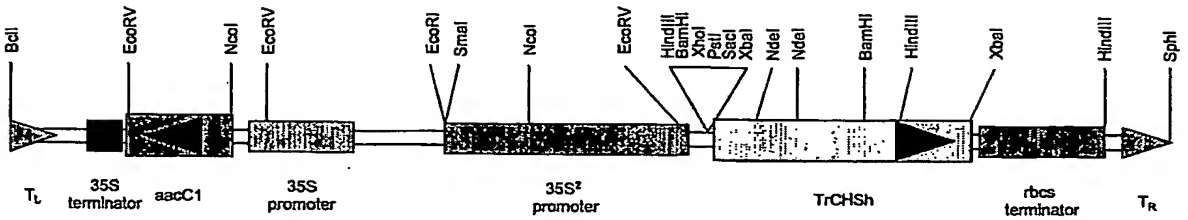

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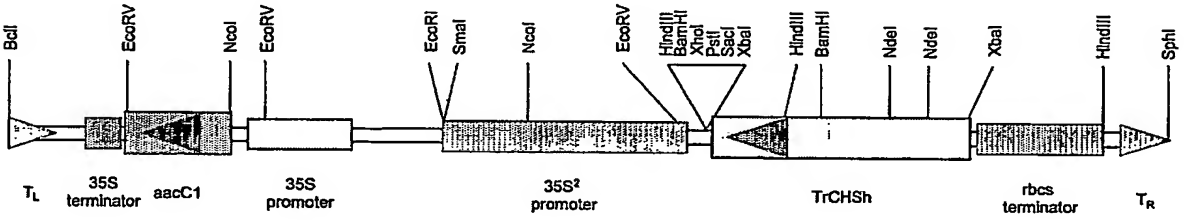

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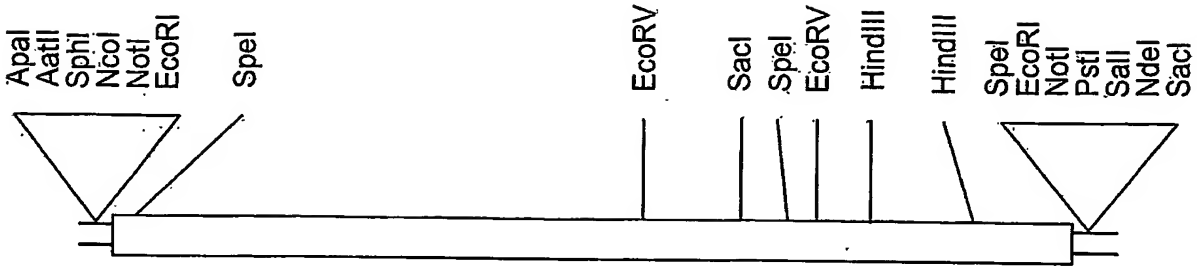
FIGURE 16



TrBANa

FIGURE 17

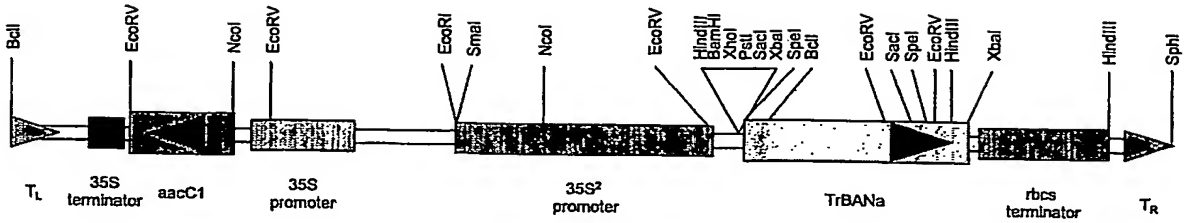
```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG ATAAAAACTG
  51 CACTAGTGTG TATAAGTTTC TTGGTGAAAA AAGAGTTTGT AAATTAACAT
 101 CATGGCTAGT ATCAAACAAA TTGGAAACAA GAAAGCATGT GTGATTGGTG
 151 GCACTGGTTT TGTTGCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
 201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAATATC
 251 TCACCTAGTG GCACTGCAAA GTTTGGGGGA ACTGAATCTA TTTAGAGCAG
 301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACTT
 351 GTTTTTCAAC TTGCTACACC TGTGAACTTT GCTTCTCAAG ATCCTGAGAA
 401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
 451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
 501 GCGGTGACTA TAAATGAACT CAAAGGGACA GGTCATGTTA TGGATGAAAC
 551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
 601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
 651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACTGG
 701 TCCTTCTCTC ACACCAGATA TCCCATCTAG TGTTGGCTTG GCAATGTCTC
 751 TAATAACAGG CAATGATTTT CTCATAAATG CTTTGAAAGG AATGCAGTTT
 801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
 851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGGTAGATAC ATTTGCTGTG
 901 CTCACAATAC TAGTGTTCCC GAGCTTGCAA AGTTTCTCAA CAAACGATAT
 951 CCTCAGTATA AAGTTCCAAC TGAATTTGAT GATTGCCCCA GCAAGGCAAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTTGATATTT CTAATTCAAT AGCAAACTCT
1151 AAGCTTGTTA TGTGTTTGTG AAGTTCAGAG TGAAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAATAAGAG GAGAGCACAA TAATTTTGGA AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1301 AGTGAATTC
```

FIGURE 18

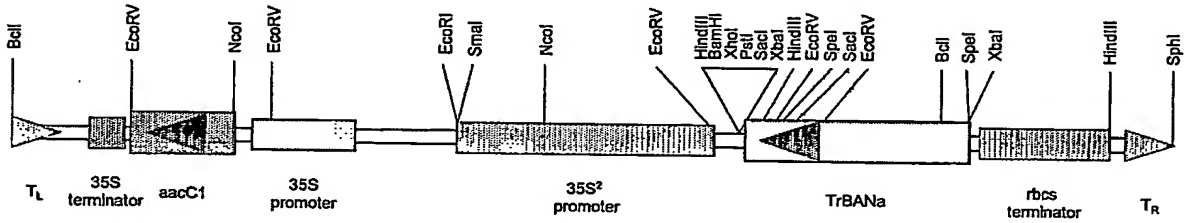
```
  1 MASIKQIGNK KACVIGGTGF VASMLIKQLL EKGYAVNTTV RDPDSPKKIS
 51 HLVALQSLGE LNLFRADLTV EEDFDAPIAG CELVFQLATP VNFASQDPEN
101 DMIKPAIKGV LNVLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDET
151 NWSDVEFLNT AKPPTWGYPA SKMLAEKAAW KFAEENDIDL ITVIPSLTTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAKFLN KRYPQYKVPT EFDDCPSKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTVEYF KTKGALKN
```

FIGURE 19

21/40



pPZP221:35S²TrBANa sense



pPZP221:35S²TrBANa anti

FIGURE 20

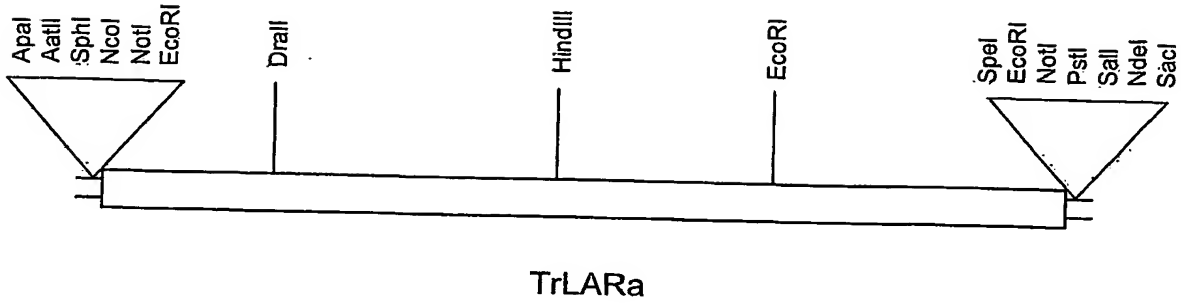

ApaI
AatII
SphI
NcoI
NotI
EcoRI
DraII
HindIII
EcoRI
SpeI
EcoRI
NotI
PstI
SalI
NdeI
SacI
TrLARa

FIGURE 21

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATACCAACA
  51 TTGTCACAAT TAACTCTAAA AGCAAAGCAA TGGCACCAGC AGCAACATCA
 101 TCACCAACCA CTCCTACTAC TACCAAGGGT CGTGTCCTAA TTGTTGGAGG
 151 AACAGGTTTC ATTGGAAAAT TTGTAACTGA GGCAAGTCTT TCCACAACAC
 201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
 251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
 301 GGTAAATAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
 351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
 401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTTGCC
 451 TTCGGAATTT GGTCACGATG TGGACAGAGC AAATCCTGTG GAACCTGGCC
 501 TAACAATGTA CAAACAGAAA CGTTTGGTTA GACGTGTGAT CGAAGAATCT
 551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
 601 CTATGACAAT TGTCATCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
 651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
 701 ATTGGGAAAT TCACAATGAA GGTCATTGAT GATGAAAGAA CAATCAACAA
 751 AAATGTTCAT TTTCGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
 801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCTAG AGTGATCGTC
 851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
 901 TGTCGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
 951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCGGCTGAC AAGATTCATA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCTGTTGA
1151 AAAGGTTCAC CTGAGGTGGA TATTCTTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTTCAAGAA TGTTTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATTGAGGTA AAAGTCTTCA TGTTTACAAA AAAAAAAAAA
1351 AAAAAAAAAA AAAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1401 AGTGAATTC
```

FIGURE 22

```
  1 MAPAATSSPT TPTTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
 51 PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC
```

FIGURE 23

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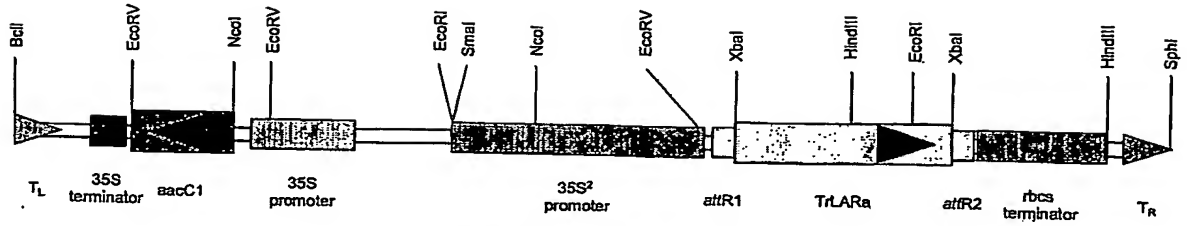
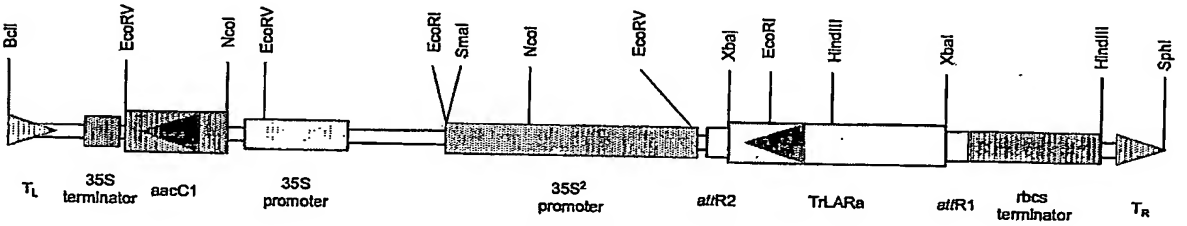


pPZP221:35S²TrLARa sense



pPZP221:35S²TrLARa anti

FIGURE 24

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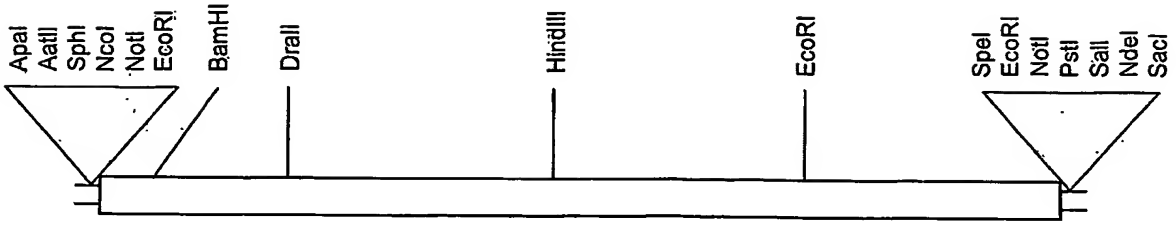


TrLARb

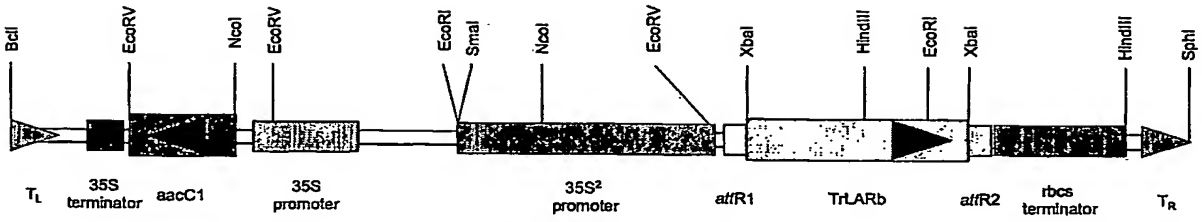
FIGURE 25

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG AGGATCCTTC
  51 CATTTTGCAT ACCAACATTG TCACAATTAA CTCTAAAAGC AAAGCAATGG
 101 CACCAGCAGC AACATCATCA CCAACCACTC CTACTACTAC CAAGGGTCGT
 151 GTCCTAATTG TTGGAGGAAC AGGTTTCATT GGAAAATTTG TAACTGAGGC
 201 AAGTCTTTCC ACAACACACC CAACCTACTT GTTGGTTCGG CCAGGACCTC
 251 TTCTCTCTTC TAAGGCTGCC ACTATTAAGG CATTCCAAGA GAAAGGTGCC
 301 ATTGTCATTT ATGGTCGGGT AAATAATAAG GAGTTCATGG AGATGATTTT
 351 GAAAAAGTAT GAGATAAATG TAGTCATTTC TGCAATAGGA GGCTCTGATG
 401 GCTTGCTGGA ACAGCTTACT TTGGTGGAGG CCATGAAATC TATTAACACC
 451 ATTAAGAGGT TTTTGCCTTC AGAATTTGGT CACGATGTGG ACAGAGCAAA
 501 TCCTGTGGAA CCTGGCCTAA CAATGTACAA ACAGAAACGT TTGGTTAGAC
 551 GTGTGATCGA AGAATCTGGT GTACCATACA CCTACATCTG TTGCAATTCG
 601 ATCGCATCCT GGCCGTACTA TGACAATTGT CATCCATCAC AGCTTCCTCC
 651 ACCGTTGGAT CAATTACATA TTTATGGTCA TGGCGATGTC AAAGCTTACT
 701 TTGTTGATGG CTATGATATT GGGAAATTCA CAATGAAGGT CATTGATGAT
 751 GAAAGAACAA TCAACAAAAA TGTTCATTTT CGACCTTCTA ACAATTGTTA
 801 TAGCATGAAT GAGCTTGCTT CTTTGTGGGA AAACAAAATT GCACGAAAAA
 851 TTCCTAGAGT GATCGTCTCT GAAGACGATC TTCTAGCAAT AGCCGCAGAA
 901 AACTGCATAC CGGAAAGTGT TGTGGCATCA ATCACTCATG ATATATTCAT
 951 CAATGGATGT CAAGTTAACT TCAAGGTAGA TGGAATTCAT GATGTTGAAA
1001 TTGGCACTCT ATATCCTGGT GAATCGGTAA GAAGTTTGGA GGAATGCTAT
1051 GAGAAATTTG TTGTCATGGC GGCTGACAAG ATTCATAAAG AAGAAACTGG
1101 AGTTACCGCA GGTGGGGGCG GCACAACGGC TATGGTAGAG CCGGTGCCAA
1151 TCACAGCTTC CTGTTGAAAA GGTTCACCTG AGGTGGATAT TCTTTTGAGT
1201 CATAAGACAT GTTGATTGTT GATGTTGTTT TCAAGAATGT TTCATCATTT
1251 CATGTGTTTT ATTAATCCTA AGTACAAATA ATTGCTGTCT ACGTACGTTC
1301 TTAGTTGCGA AAATTCTTGT TATTCTCTAT TGGGGTAAAA GTCTTCATGT
1351 TTATTGTAGT TGTGTTGGTT TTTCATATAT GCTATTTGCA ATAATGATTT
1401 TTGTGAAGCA CTTGTGGTGT ATTTACTTAC TACTGAAAAT AATGGTTACA
1451 CAAAATATAT AAAAAAATAA AAATAAGCAA AAAAAAAAAA AAAAAAAAAA
1501 AAAAAAAAAA GTACTCTGCG TTGTTACCAC TGCTTAATCA CTAGTGAATT
1551 C
```

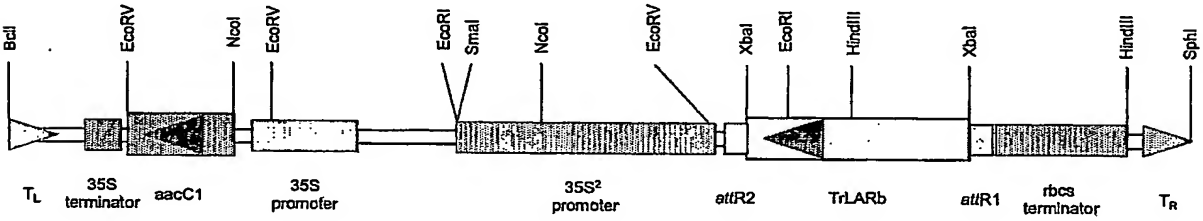
FIGURE 26

```
  1  MAPAATSSPT TPTTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
 51  PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101  DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRANPVEPG LTMYKQKRLV
151  RRVIEESGVP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201  YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251  KIPRVIVSED DLLAIAAENC IPESVVASIT HDIFINGCQV NFKVDGIHDV
301  EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351  PITASC
```

FIGURE 27

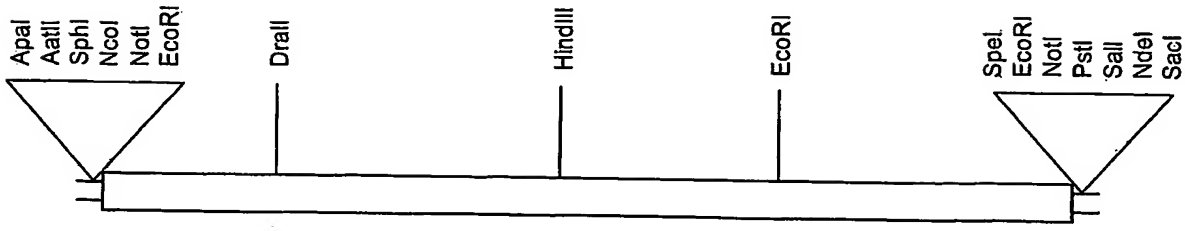


pPZP221:35S²TrLARb sense



pPZP221:35S²TrLARb anti

FIGURE 28



TrLARc

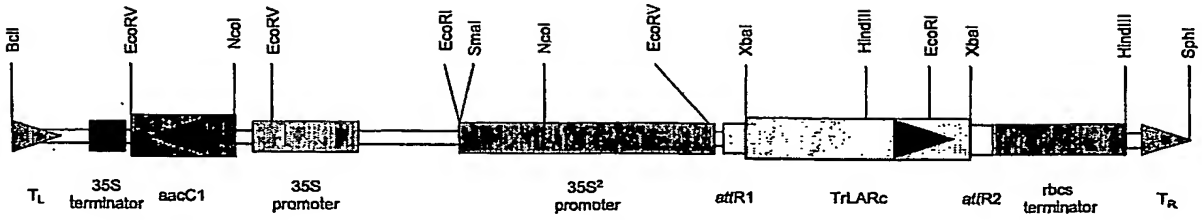
FIGURE 29

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATACCAACA
  51 TTGTCACAAT TAACTCTAAA AGTAAAGCAA TGGCACCAGC AGCAACATCA
 101 TCACCAACCA CTCCCACTAC TACCAAGGGT CGTGTCCTAA TTGTTGGAGG
 151 AACAGGTTTC ATTGGAAAAT TTGTAACTGA GGCAAGTCTT TCCACAACAC
 201 ACCCAACCTA CTTGTTGGTT CGGCCAGGAC CTCTTCTCTC TTCTAAGGCT
 251 GCCACTATTA AGGCATTCCA AGAGAAAGGT GCCATTGTCA TTTATGGTCG
 301 GGTAAATAAT AAGGAGTTCA TGGAGATGAT TTTGAAAAAG TATGAGATAA
 351 ATGTAGTCAT TTCTGCAATA GGAGGCTCTG ATGGCTTGCT GGAACAGCTT
 401 ACTTTGGTGG AGGCCATGAA ATCTATTAAC ACCATTAAGA GGTTTTTGCC
 451 TTCGGAATTT GGTCACGATG TGGACAGAGC AGATCCTGTG GAACCTGGCC
 501 TAACAATGTA CAAACAGAAA CGTTTGGTTA GACGTGTGAT CGAAGAATCT
 551 GGTATACCAT ACACCTACAT CTGTTGCAAT TCGATCGCAT CTTGGCCGTA
 601 CTATGACAAT TGTCATCCAT CACAGCTTCC TCCACCGTTG GATCAATTAC
 651 ATATTTATGG TCATGGCGAT GTCAAAGCTT ACTTTGTTGA TGGCTATGAT
 701 ATTGGGAAAT TCACAATGAA GGTCATTGAT GATGAAAGAA CAATCAACAA
 751 AAATGTTCAT TTTCGACCTT CTAACAATTG TTATAGCATG AATGAGCTTG
 801 CTTCTTTGTG GGAAAACAAA ATTGCACGAA AAATTCCTAG AGTGATCGTC
 851 TCTGAAGACG ATCTTCTAGC AATAGCCGCA GAAAATTGCA TACCGGAAAG
 901 TGTCGTGGCA CCAATCACTC ATGATATATT CATCAATGGA TGTCAAGTTA
 951 ACTTCAAGAT AGATGGAATT CATGATGTTG AAATTGGCAC TCTATATCCT
1001 GGTGAATCGG TAAGAAGTTT GGAGGAATGC TATGAGAAAT TTGTTGTCAT
1051 GGCGGCTGAC AAGATTCATA AAGAAGAAAC TGGAGTTACC GCAGGTGGGG
1101 GCGGCACAAC GGCTATGGTA GAGCCGGTGC CAATCACAGC TTCCTGTTGA
1151 AAAGGTTCAC CTGAGGTGGA TATTCTTTTG AGTCATAAGA CATGTTGATT
1201 GTTGATGTTG TTTTCAAGAA TGTTTCATCA TTTCATGTGT TTTATTAATC
1251 CTAAGTACAA ATAATTGCTG TCTACGTACG TTCTTAGTTG CAAAAATTCT
1301 TGTTATTCTC TATCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAGTACTCT
1351 GCGTTGTTAC CACTGCTTAA TCACTAGTGA ATTC
```

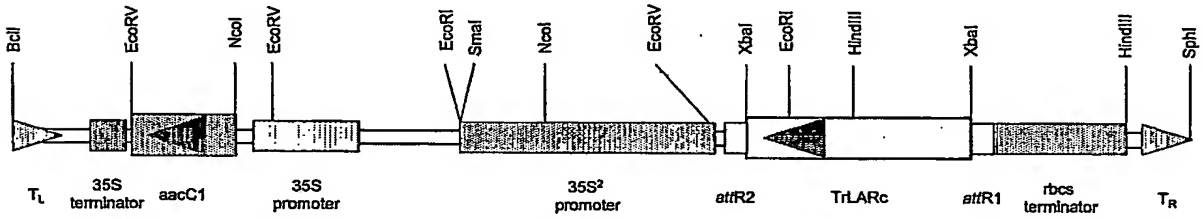
FIGURE 30

```
  1 MAPAATSSPT TPTTTKGRVL IVGGTGFIGK FVTEASLSTT HPTYLLVRPG
 51 PLLSSKAATI KAFQEKGAIV IYGRVNNKEF MEMILKKYEI NVVISAIGGS
101 DGLLEQLTLV EAMKSINTIK RFLPSEFGHD VDRADPVEPG LTMYKQKRLV
151 RRVIEESGIP YTYICCNSIA SWPYYDNCHP SQLPPPLDQL HIYGHGDVKA
201 YFVDGYDIGK FTMKVIDDER TINKNVHFRP SNNCYSMNEL ASLWENKIAR
251 KIPRVIVSED DLLAIAAENC IPESVVAPIT HDIFINGCQV NFKIDGIHDV
301 EIGTLYPGES VRSLEECYEK FVVMAADKIH KEETGVTAGG GGTTAMVEPV
351 PITASC
```

FIGURE 31

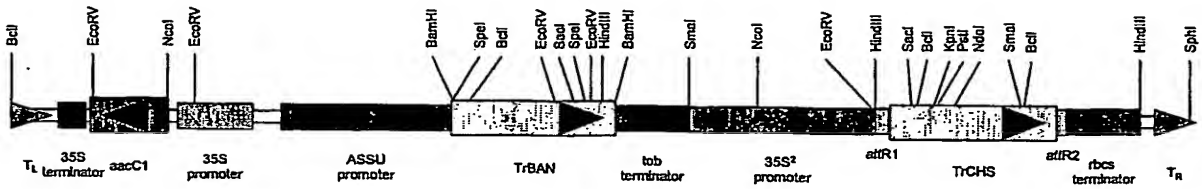


pPZP221:35S²TrLARc sense



pPZP221:35S²TrLARc anti

FIGURE 32



pPZP221:ASSU::BAN:35S²::CHS

FIGURE 33

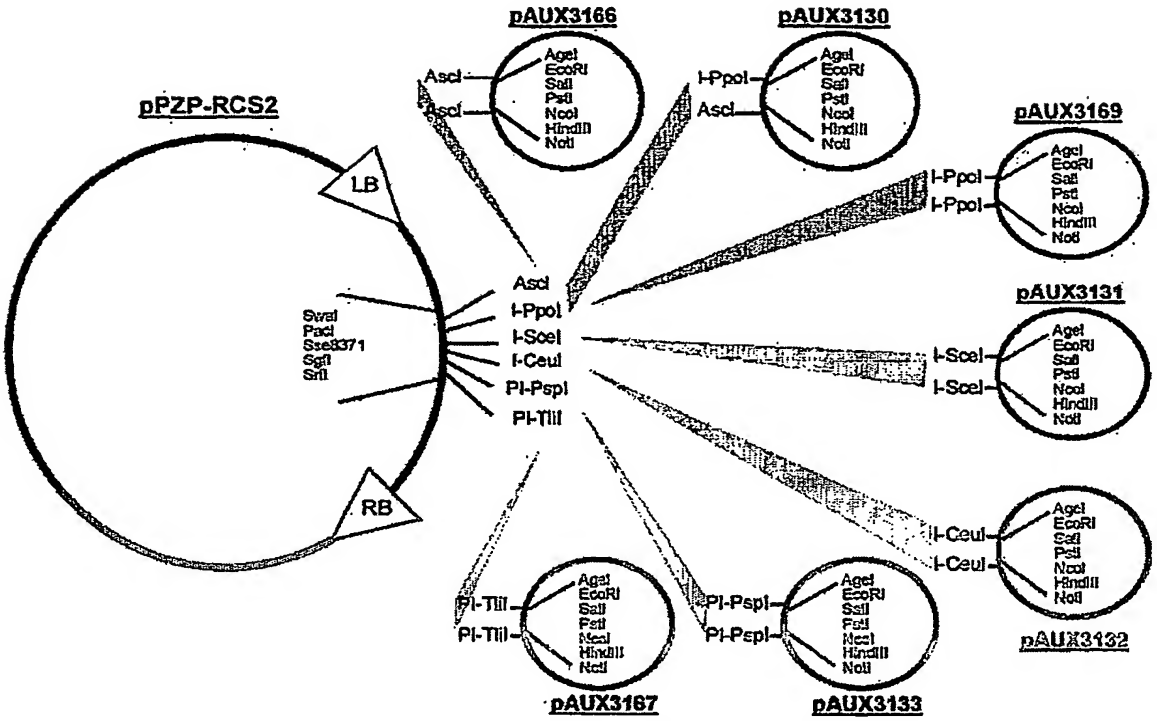
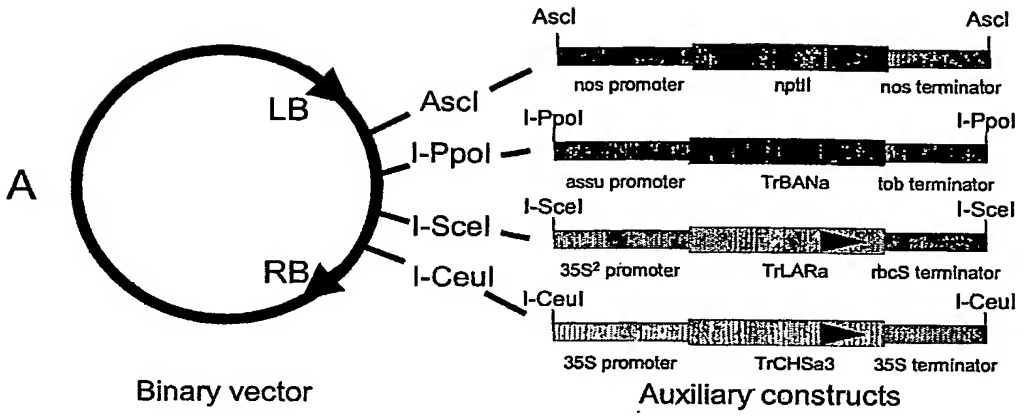

pPZP-RCS2
LB
RB
SwaI
PacI
Sse8371
SgfI
SrfI
AscI
I-PpoI
I-SceI
I-CeuI
PI-PspI
PI-TliI
pAUX3166
pAUX3130
pAUX3169
pAUX3131
pAUX3132
pAUX3167
pAUX3133
AgeI
EcoRI
SalI
PstI
NcoI
HindIII
NotI

FIGURE 34


A
LB
RB
AscI
I-PpoI
I-SceI
I-CeuI
Binary vector
AscI
AscI
nos promoter
nptII
nos terminator
I-PpoI
I-PpoI
assu promoter
TrBANa
tob terminator
I-SceI
I-SceI
35S² promoter
TrLARa
rbcS terminator
I-CeuI
I-CeuI
35S promoter
TrCHSa3
35S terminator
Auxiliary constructs

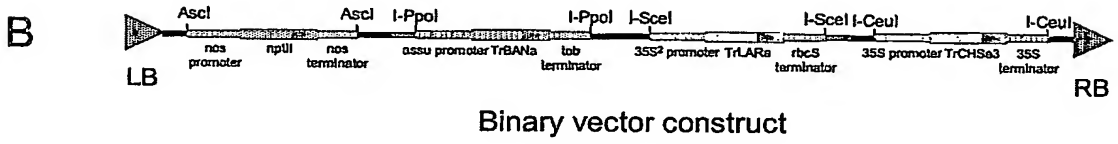

B
LB
AscI
nos promoter
nptII
nos terminator
AscI
I-PpoI
assu promoter TrBANa
tob terminator
I-PpoI
I-SceI
35S² promoter TrLARa
rbcS terminator
I-SceI
I-CeuI
35S promoter TrCHSa3
35S terminator
I-CeuI
RB
Binary vector construct

FIGURE 35

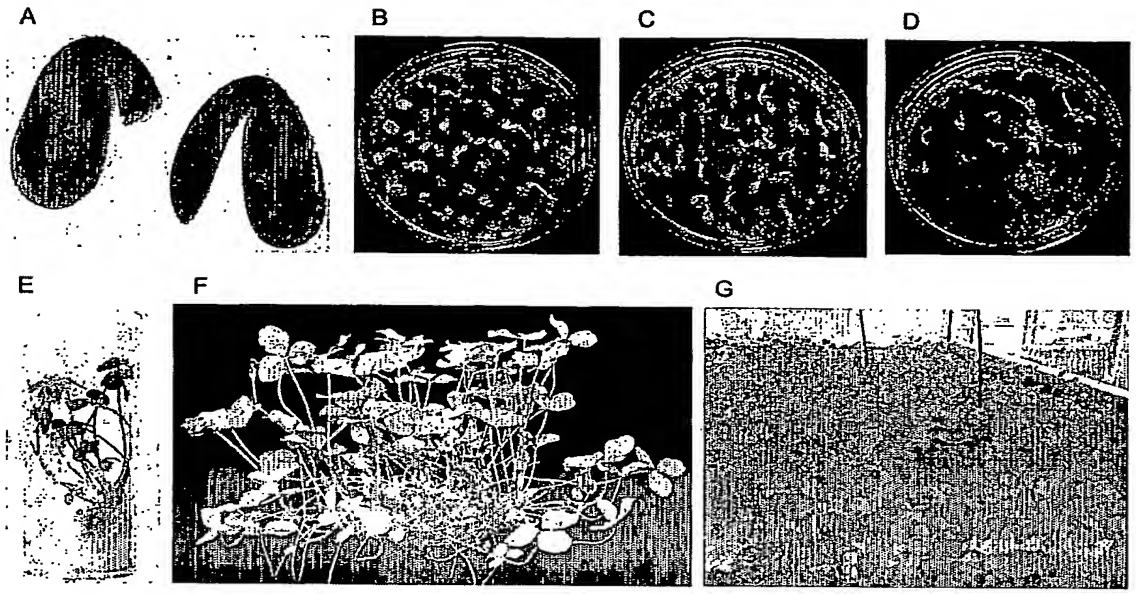


FIGURE 36

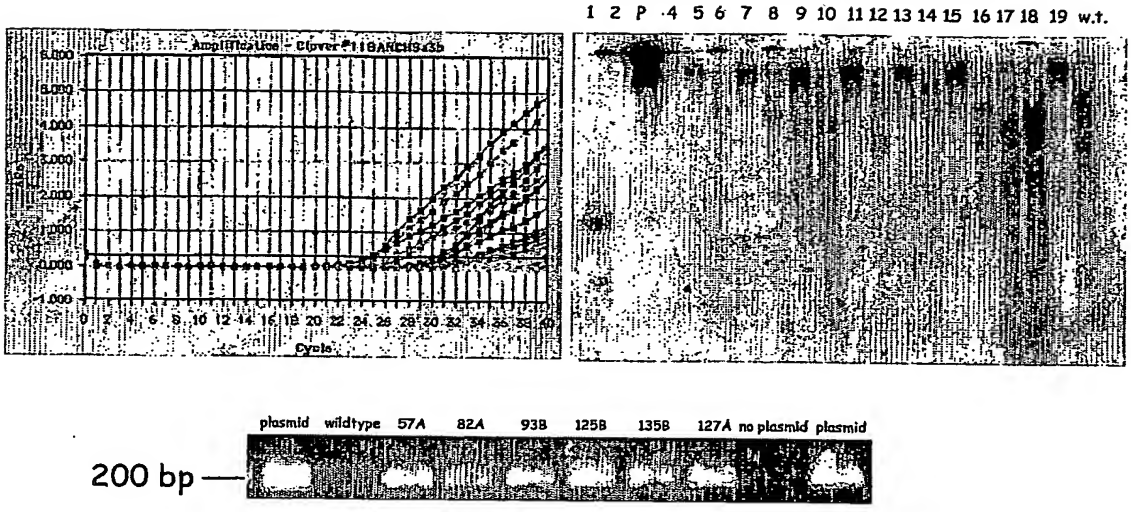
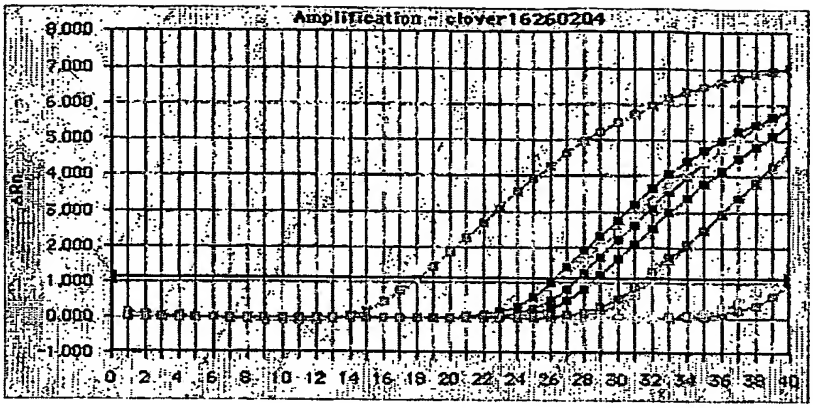

1 2 P 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 w.t.
Cycle
plasmid wildtype 57A 82A 93B 125B 135B 127A no plasmid plasmid
200 bp

FIGURE 37



1Kb+ 3A 22A 6B 24A 34A 29E Blank W.T. P

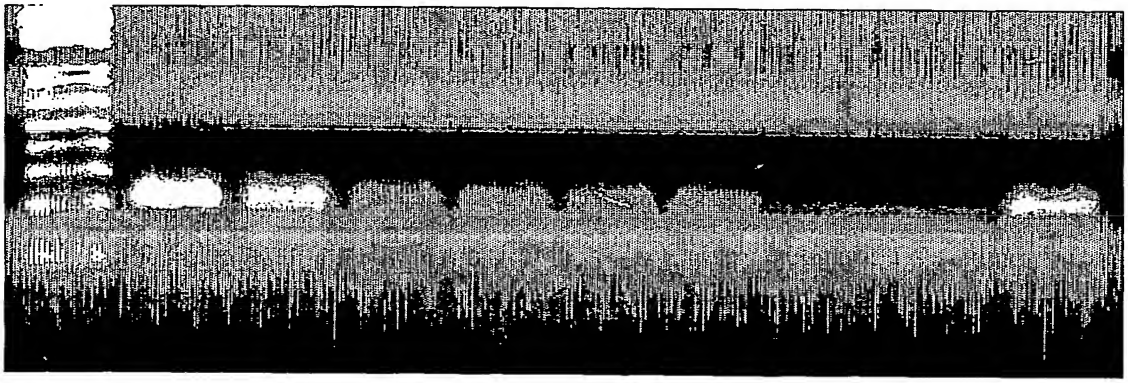
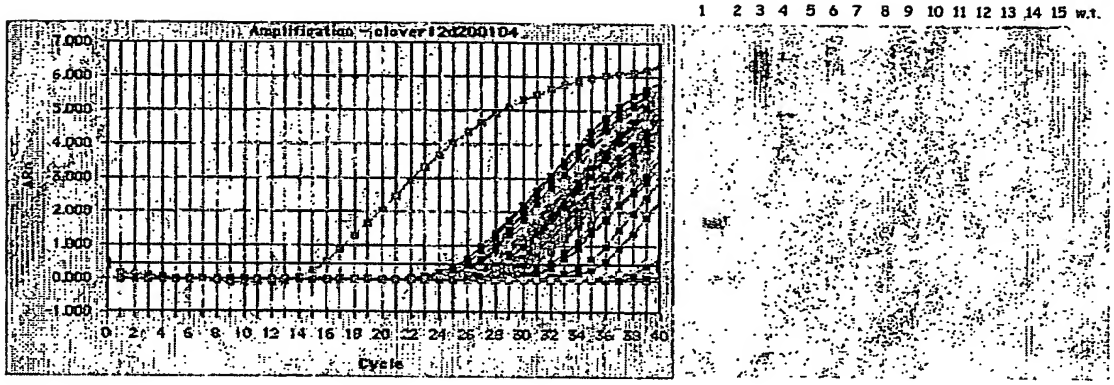


FIGURE 38

40/40



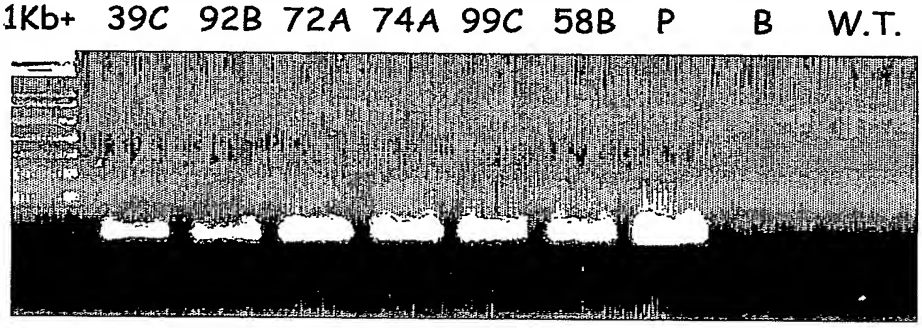


FIGURE 39

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